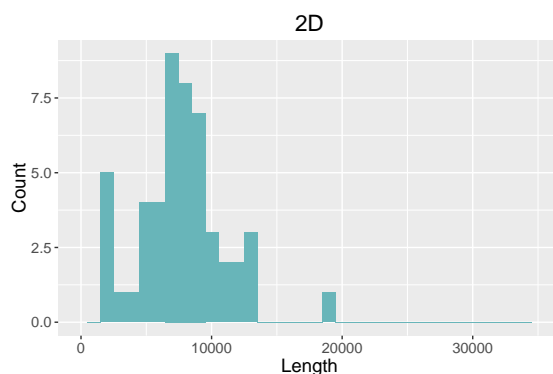


NanoOK report for nanook

Read lengths

Type	NumReads	TotalBases	Mean	Longest	Shortest	N50	N50Count	N90	N90Count
2D	50	387675	7753.50	19041	1620	8540	18	5558	39



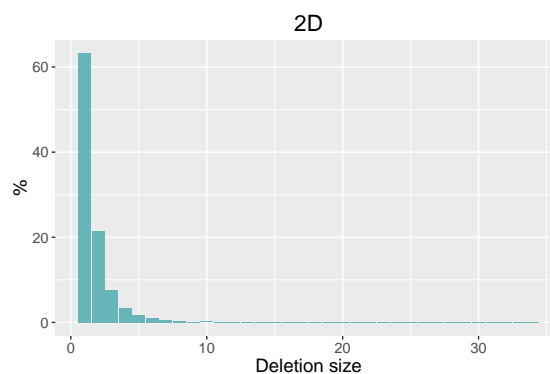
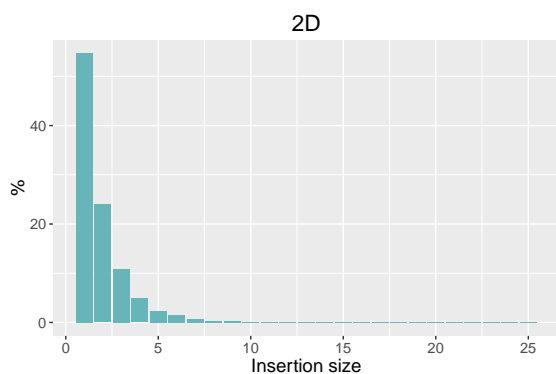
2D alignments

Number of reads	50
Number of reads with alignments	50 (100.00%)
Number of reads without alignments	0 (0.00%)

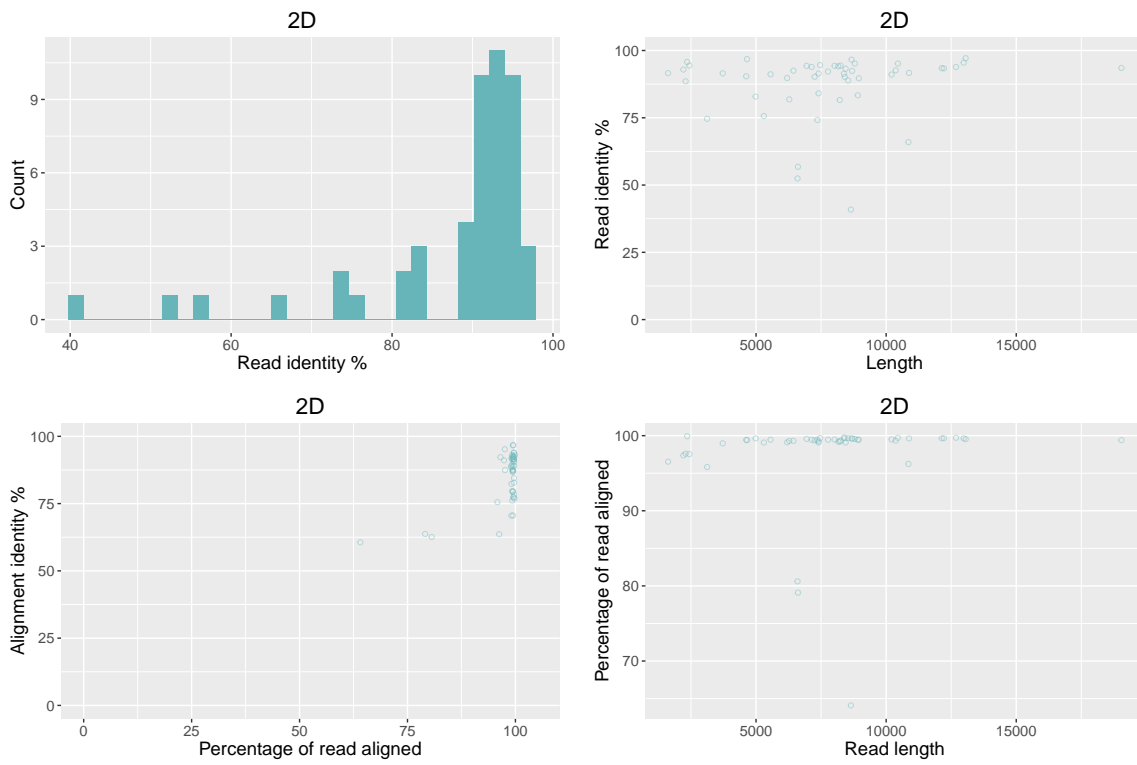
ID	Size	Number of Reads	% of Reads	Mean read length	Aligned bases	Mean coverage	Longest Perf Kmer
Escherichia coli	4641652	50	100.00	7753.50	399524	0.09	343

Escherichia coli error analysis

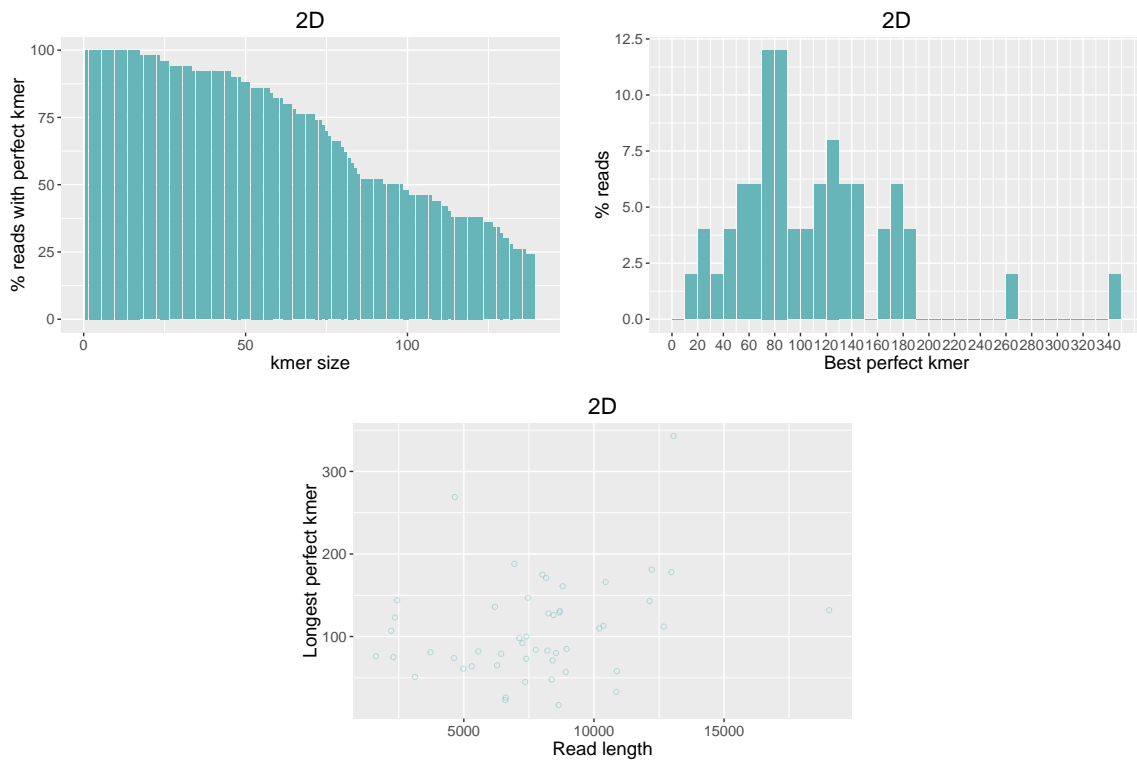
	2D
Overall base identity (excluding indels)	88.17%
Aligned base identity (excluding indels)	94.16%
Identical bases per 100 aligned bases (including indels)	85.56%
Inserted bases per 100 aligned bases (including indels)	4.09%
Deleted bases per 100 aligned bases (including indels)	5.05%
Substitutions per 100 aligned bases (including indels)	5.30%
Mean insertion size	1.93
Mean deletion size	1.72



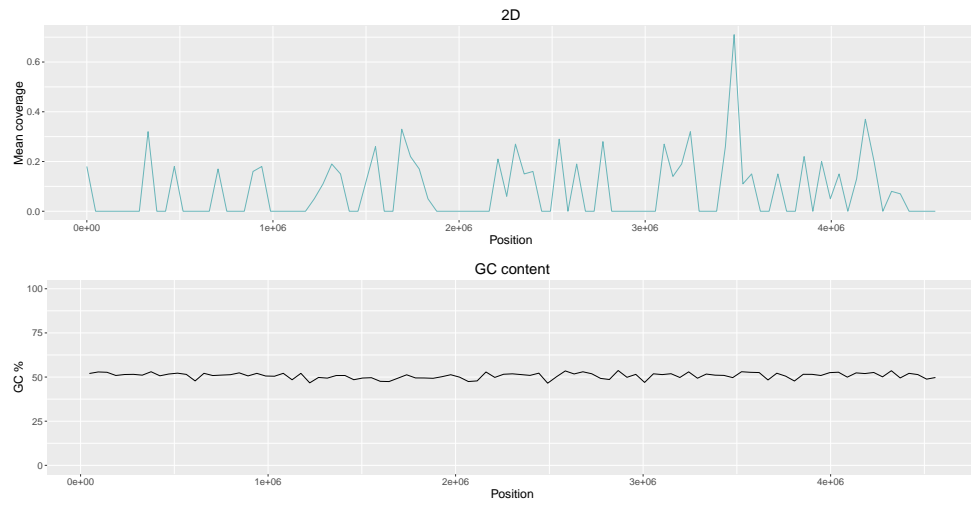
Escherichia coli read identity



Escherichia coli perfect kmers



Escherichia coli coverage



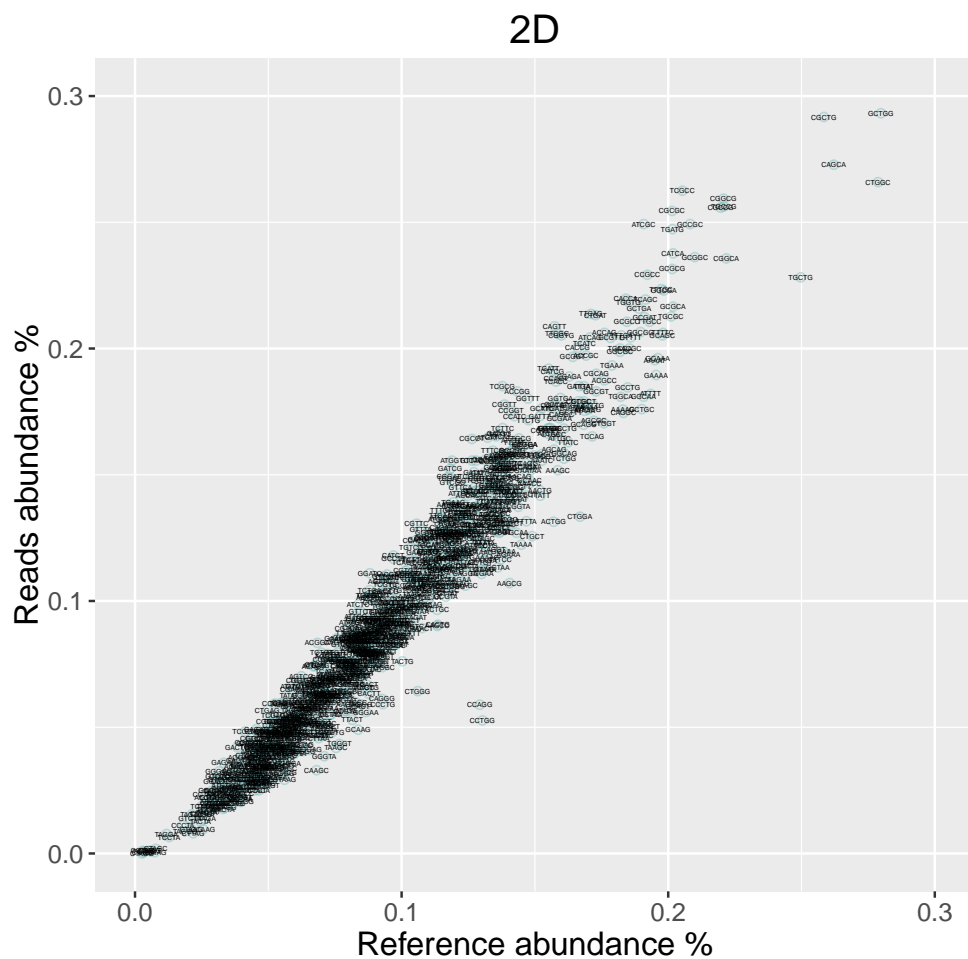
Escherichia coli 5-mer analysis

Under-represented 5-mers

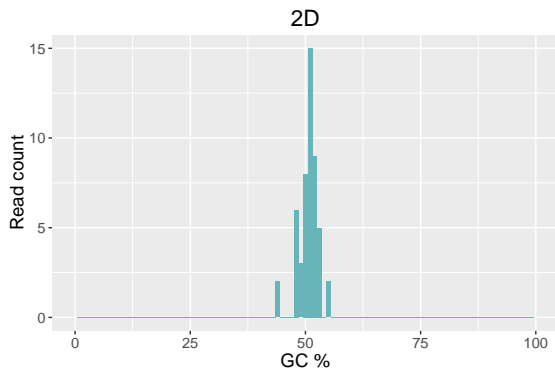
Rank	kmer	2D		
		Ref %	Read %	Diff %
1	CCTGG	0.130	0.053	-0.078
2	CCAGG	0.129	0.059	-0.070
3	CTGGG	0.106	0.064	-0.042
4	CAAGC	0.068	0.033	-0.035
5	GCAAG	0.084	0.049	-0.035
6	CCCTG	0.093	0.059	-0.034
7	TAAGC	0.075	0.042	-0.034
8	CTGGA	0.167	0.133	-0.033
9	AAGCG	0.141	0.107	-0.033
10	TGGGT	0.077	0.043	-0.033

Over-represented 5-mers

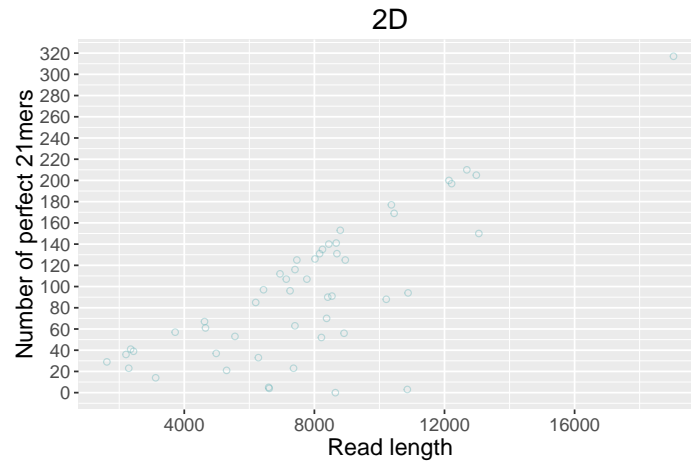
Rank	kmer	2D		
		Ref %	Read %	Diff %
1	TTTTT	0.251	0.619	0.368
2	AAAAA	0.247	0.575	0.328
3	ATCGC	0.191	0.249	0.059
4	TCGCC	0.205	0.263	0.057
5	CGCGC	0.201	0.255	0.053
6	CCAGC	0.288	0.340	0.052
7	CAGTT	0.157	0.209	0.051
8	CAGCG	0.262	0.313	0.051
9	CGCCA	0.288	0.337	0.049
10	TTCGC	0.158	0.206	0.048



Escherichia coli GC content



All reference 21mer analysis









All reference substitutions

		2D substituted %			
		a	c	g	t
Reference	A	0.00	5.98	13.64	5.57
	C	6.58	0.00	4.33	14.35
	G	12.52	4.51	0.00	6.17
	T	5.82	14.58	5.96	0.00

Kmer motifs before errors

3-mer error motif analysis







Rank	2D		
	Insertion	Deletion	Substitution
1	TTC (3.28%)	CGC (3.35%)	CGC (4.40%)
2	ATC (3.24%)	TTT (3.26%)	TTT (4.02%)
3	CGC (3.19%)	ATC (3.16%)	GCC (3.96%)
4	GCC (2.93%)	GCC (2.76%)	ATC (3.47%)
5	TTT (2.90%)	TTC (2.71%)	TGC (3.26%)
6	TGC (2.79%)	ATT (2.59%)	TTC (3.24%)
7	GGC (2.79%)	GGC (2.52%)	AAA (3.16%)
8	CTG (2.55%)	AAC (2.43%)	ACC (3.07%)
9	GCG (2.40%)	TCA (2.40%)	TCC (2.56%)
10	AGC (2.22%)	GTT (2.34%)	ATT (2.41%)
			
-10	TGT (0.86%)	TAA (0.90%)	GTA (0.74%)
-9	GAG (0.84%)	CCT (0.87%)	ACT (0.72%)
-8	AGT (0.82%)	AGT (0.84%)	ACA (0.68%)
-7	AGA (0.82%)	GAG (0.82%)	GGA (0.68%)
-6	TAA (0.80%)	GGA (0.82%)	GGG (0.61%)
-5	GTA (0.75%)	GTA (0.60%)	AGG (0.59%)
-4	GGA (0.56%)	GGG (0.53%)	GAG (0.44%)
-3	GGG (0.55%)	AGG (0.47%)	AGT (0.40%)
-2	CTA (0.31%)	TAG (0.37%)	TAG (0.21%)
-1	TAG (0.31%)	CTA (0.21%)	CTA (0.15%)
			

Most common

Least common

Kmer space for 3-mers: 64 Random chance for any given 3-mer: 1.56%

4-mer error motif analysis

Rank	2D		
	Insertion	Deletion	Substitution
1	CGCC (1.31%)	CGCC (1.31%)	TTTT (1.66%)
2	TTTC (1.05%)	CAGC (1.14%)	CGCC (1.63%)
3	CGGC (1.03%)	TTTC (1.13%)	AAAA (1.58%)
4	TGCC (1.01%)	ATTT (1.06%)	GCGC (1.48%)
5	CTGC (0.99%)	GCGC (1.02%)	CATC (1.19%)
6	CAGC (0.97%)	GTTT (1.02%)	TGCC (1.19%)
7	CTTC (0.97%)	ACGC (0.95%)	ACGC (1.16%)
8	ATCC (0.95%)	AATC (0.94%)	TTTC (1.16%)
9	TCGC (0.91%)	CATC (0.90%)	ATCC (1.09%)
10	CATC (0.91%)	TTCA (0.90%)	CTGC (1.06%)
			
-10	CCTA (0.08%)	GCTA (0.07%)	GAGG (0.05%)
-9	ATAG (0.08%)	CTAA (0.07%)	CAAG (0.05%)
-8	TTAG (0.08%)	CTTG (0.07%)	TCTA (0.02%)
-7	AGGA (0.06%)	AGGG (0.05%)	TAGG (0.02%)
-6	TCTA (0.06%)	TCTA (0.05%)	TAGA (0.02%)
-5	CTCG (0.06%)	TAAG (0.05%)	GCTA (0.02%)
-4	TAGA (0.06%)	TAGG (0.04%)	GAGT (0.02%)
-3	GGGA (0.06%)	CTTA (0.03%)	CCTA (0.02%)
-2	AGGG (0.02%)	CTAG (0.01%)	CTTA (0.02%)
-1	TAGT (0.02%)	CCTA (0.01%)	GGAG (0.02%)
			

Most common

Least common

Kmer space for 4-mers: 256 Random chance for any given 4-mer: 0.39%

5-mer error motif analysis

Rank	2D		
	Insertion	Deletion	Substitution
1	ACGCC (0.46%)	CCAGC (0.50%)	TTTTT (0.76%)
2	GCTGC (0.42%)	CGCCA (0.46%)	AAAAA (0.76%)
3	CCAGC (0.40%)	TCGCC (0.44%)	GGCGC (0.54%)
4	AACTG (0.38%)	GATTT (0.41%)	ACGCC (0.54%)
5	ATCGC (0.38%)	ATTTT (0.41%)	CAGCC (0.51%)
6	CGCCA (0.38%)	AAATC (0.38%)	TTGCC (0.48%)
7	TATTC (0.35%)	TCACC (0.38%)	AAATT (0.45%)
8	ATTTT (0.35%)	CGTTT (0.38%)	CCACC (0.45%)
9	GCCAG (0.35%)	AACGC (0.35%)	CCGCC (0.45%)
10	TTTCT (0.35%)	GCTGG (0.34%)	CTGCC (0.45%)
-10	ACTCC (0.02%)	TACTA (0.01%)	CCCTT (0.03%)
-9	GTGTG (0.02%)	TTGGG (0.01%)	GTGTG (0.03%)
-8	GTGTA (0.02%)	ACAAG (0.01%)	CCCTC (0.03%)
-7	GTAGT (0.02%)	GTGTG (0.01%)	GTAGT (0.03%)
-6	GAGGA (0.02%)	CCCTA (0.01%)	GTAGA (0.03%)
-5	AGTTG (0.02%)	GAGGG (0.01%)	TTGAG (0.03%)
-4	GTAGG (0.02%)	GAGGC (0.01%)	ACTAC (0.03%)
-3	GTAGA (0.02%)	GTAGC (0.01%)	AGCAG (0.03%)
-2	AGCAC (0.02%)	ACTAA (0.01%)	ACGGG (0.03%)
-1	ACGGA (0.02%)	GCACA (0.01%)	ACGGA (0.03%)

Most common

Least common

Kmer space for 5-mers: 1024 Random chance for any given 5-mer: 0.10%